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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/487,792

DATE: 02/11/2000
TIME: 09:39:02

Input Set: I487792.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

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1 <110> APPLICANT: Human Genome Sciences, Inc.
2 <120> TITLE OF INVENTION: Keratinocyte Derived Interferon
3 <130> FILE REFERENCE: PF482P1
4 <140> CURRENT APPLICATION NUMBER: US/09/487,792
5 <141> CURRENT FILING DATE: 2000-01-20
6 <150> EARLIER APPLICATION NUMBER: 60/093,643
7 <151> EARLIER FILING DATE: 1998-07-21
8 <150> EARLIER APPLICATION NUMBER: PCT/US99/16424
9 <151> EARLIER FILING DATE: 1999-07-21
10 <160> NUMBER OF SEQ ID NOS: 54
11 <170> SOFTWARE: PatentIn Ver. 2.1
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14 <212> TYPE: DNA
15 <213> ORGANISM: Homo sapiens
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22                                     1               5
23 att caa aag tgt ttg tgg ctt gag atc ctt atg ggt ata ttc att gct 103
24 Ile Gln Lys Cys Leu Trp Leu Glu Ile Leu Met Gly Ile Phe Ile Ala
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26 ggc acc cta tcc ctg gac tgt aac tta ctg aac gtt cac ctg aga aga 151
27 Gly Thr Leu Ser Leu Asp Cys Asn Leu Leu Asn Val His Leu Arg Arg
28             25               30               35
29 gtc acc tgg caa aat ctg aga cat ctg agt agt atg agc aat tca ttt 199
30 Val Thr Trp Gln Asn Leu Arg His Leu Ser Ser Met Ser Asn Ser Phe
31             40               45               50               55
32 cct gta gaa tgt cta cga gaa aac ata gct ttt gag ttg ccc caa gag 247
33 Pro Val Glu Cys Leu Arg Glu Asn Ile Ala Phe Glu Leu Pro Gln Glu
34             60               65               70
35 ttt ctg caa tac acc caa cct atg aag agg gac atc aag aag gcc ttc 295
36 Phe Leu Gln Tyr Thr Gln Pro Met Lys Arg Asp Ile Lys Lys Ala Phe
37             75               80               85
38 tat gaa atg tcc cta cag gcc ttc aac atc ttc agc caa cac acc ttc 343
39 Tyr Glu Met Ser Leu Gln Ala Phe Asn Ile Phe Ser Gln His Thr Phe
40             90               95              100
41 aaa tat tgg aaa gag aga cac ctc aaa caa atc caa ata gga ctt gat 391
42 Lys Tyr Trp Lys Glu Arg His Leu Lys Gln Ile Gln Ile Gly Leu Asp
43             105              110              115
44 cag caa gca gag tac ctg aac caa tgc ttg gag gaa gac gag aat gaa 439

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45      Gln Gln Ala Glu Tyr Leu Asn Gln Cys Leu Glu Glu Asp Glu Asn Glu
46      120                      125                      130                      135
47      aat gaa gac atg aaa gaa atg aaa gag aat gag atg aaa ccc tca gaa      487
48      Asn Glu Asp Met Lys Glu Met Lys Glu Asn Glu Met Lys Pro Ser Glu
49                      140                      145                      150
50      gcc agg gtc ccc cag ctg agc agc ctg gaa ctg agg aga tat ttc cac      535
51      Ala Arg Val Pro Gln Leu Ser Ser Leu Glu Leu Arg Arg Tyr Phe His
52                      155                      160                      165
53      agg ata gac aat ttc ctg aaa gaa aag aaa tac agt gac tgt gcc tgg      583
54      Arg Ile Asp Asn Phe Leu Lys Glu Lys Lys Tyr Ser Asp Cys Ala Trp
55                      170                      175                      180
56      gag att gtc cga gtg gaa atc aga aga tgt ttg tat tac ttt tac aaa      631
57      Glu Ile Val Arg Val Glu Ile Arg Arg Cys Leu Tyr Tyr Phe Tyr Lys
58                      185                      190                      195
59      ttt aca gct cta ttc agg agg aaa taagaatcat ctaccttcaa gcaagaatta      685
60      Phe Thr Ala Leu Phe Arg Arg Lys
61      200                      205
62      acagagattg tggctacgca aatgcaccaa aaaagggtga aatatatctg aaatgtacct      745
63      ggttctgccc ttggaagcca cttcctgctc atgccactaa cagcatgctg ccaaactggt      805
64      cagattcaag attattccaa gcgcagggcc caaatgttat agccaaagaa agtcttatga      865
65      taaaagtgag gcaaatttca gccaaagaagt tagaagagat gtttaaaaga acaagaacaa      925
66      attgtggatc atggtatatg caggctatca gcagaaggat cagacaataa aatgagttag      985
67      tgcaaaccat ttagtaaaaa taactatcag cagagttggt ccagattaaa aatagtacta      1045
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79                      20                      25                      30
80      Leu Asn Val His Leu Arg Arg Val Thr Trp Gln Asn Leu Arg His Leu
81                      35                      40                      45
82      Ser Ser Met Ser Asn Ser Phe Pro Val Glu Cys Leu Arg Glu Asn Ile
83      50                      55                      60
84      Ala Phe Glu Leu Pro Gln Glu Phe Leu Gln Tyr Thr Gln Pro Met Lys
85      65                      70                      75                      80
86      Arg Asp Ile Lys Lys Ala Phe Tyr Glu Met Ser Leu Gln Ala Phe Asn
87                      85                      90                      95
88      Ile Phe Ser Gln His Thr Phe Lys Tyr Trp Lys Glu Arg His Leu Lys
89                      100                      105                      110
90      Gln Ile Gln Ile Gly Leu Asp Gln Gln Ala Glu Tyr Leu Asn Gln Cys
91      115                      120                      125
92      Leu Glu Glu Asp Glu Asn Glu Asn Glu Asp Met Lys Glu Met Lys Glu
93      130                      135                      140
94      Asn Glu Met Lys Pro Ser Glu Ala Arg Val Pro Gln Leu Ser Ser Leu

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95      145      150      155      160
96      Glu Leu Arg Arg Tyr Phe His Arg Ile Asp Asn Phe Leu Lys Glu Lys
97      165      170      175
98      Lys Tyr Ser Asp Cys Ala Trp Glu Ile Val Arg Val Glu Ile Arg Arg
99      180      185      190
100     Cys Leu Tyr Tyr Phe Tyr Lys Phe Thr Ala Leu Phe Arg Arg Lys
101     195      200      205
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110     20      25      30
111     Leu Ser Arg Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser
112     35      40      45
113     Pro Phe Leu Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu
114     50      55      60
115     Met Val Lys Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu
116     65      70      75      80
117     His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser
118     85      90      95
119     Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Glu Leu
120     100     105     110
121     His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly
122     115     120     125
123     Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Val Pro Gln Leu Ser Ser
124     130     135     140
125     Leu Glu Leu Arg Arg Tyr Phe His Arg Ile Asp Asn Phe Leu Lys Glu
126     145     150     155     160
127     Lys Lys Tyr Ser Asp Cys Ala Trp Glu Ile Val Arg Val Glu Ile Arg
128     165     170     175
129     Arg Cys Leu Tyr Tyr Phe Tyr Lys Phe Thr Ala Leu Pro Ala Leu Thr
130     180     185     190
131     Leu Arg Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys
132     195     200     205
133     Tyr Ser Asp Cys Ala Trp Glu Val Val Arg Met Glu Ile Met Lys Ser
134     210     215     220
135     Leu Phe Leu Ser Thr Asn Met Gln Glu Arg Leu Arg Ser Lys
136     225     230     235
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143     1      5      10      15
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145          20          25          30
146 Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg
147          35          40          45
148 Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu
149          50          55          60
150 Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile
151          65          70          75          80
152 Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser
153          85          90          95
154 Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
155          100         105         110
156 Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu
157          115         120         125
158 Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys
159          130         135         140
160 Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser
161          145         150         155         160
162 His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr
163          165         170         175
164 Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn
165          180         185
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168 <212> TYPE: PRT
169 <213> ORGANISM: Homo sapiens
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174          20          25          30
175 Val Gly Arg Lys Asn Leu Arg Leu Leu Asp Glu Met Arg Arg Leu Ser
176          35          40          45
177 Pro His Phe Cys Leu Gln Asp Arg Lys Asp Phe Ala Leu Pro Gln Glu
178          50          55          60
179 Met Val Glu Gly Gly Gln Leu Gln Glu Ala Gln Ala Ile Ser Val Leu
180          65          70          75          80
181 His Glu Met Leu Gln Gln Ser Phe Asn Leu Phe His Thr Glu His Ser
182          85          90          95
183 Ser Ala Ala Trp Asp Thr Thr Leu Leu Glu Pro Cys Arg Thr Gly Leu
184          100         105         110
185 His Gln Gln Leu Asp Asn Leu Asp Ala Cys Leu Gly Gln Val Met Gly
186          115         120         125
187 Glu Glu Asp Ser Ala Leu Gly Arg Thr Gly Pro Leu Ala Leu Lys Arg
188          130         135         140
189 Tyr Phe Gln Gly Ile His Val Tyr Leu Lys Glu Lys Gly Tyr Ser Asp
190          145         150         155         160
191 Cys Ala Trp Glu Thr Val Arg Leu Glu Ile Met Arg Ser Phe Ser Ser
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193 Leu Ile Ser Leu Gln Glu Arg Leu Arg Met Met Asp Gly Asp Leu Ser
194          180         185         190

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204          20          25          30
205      Leu Ser Arg Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser
206          35          40          45
207      Pro Phe Leu Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu
208          50          55          60
209      Met Val Lys Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu
210          65          70          75          80
211      His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser
212          85          90          95
213      Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Glu Leu
214          100         105         110
215      His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly
216          115         120         125
217      Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Val Pro Gln Leu Ser Ser
218          130         135         140
219      Leu Glu Leu Arg Arg Tyr Phe His Arg Ile Asp Asn Phe Leu Lys Glu
220          145         150         155         160
221      Lys Lys Tyr Ser Asp Cys Ala Trp Glu Ile Val Arg Val Glu Ile Arg
222          165         170         175
223      Arg Cys Leu Tyr Tyr Phe Tyr Lys Phe Thr Ala Leu Pro Ala Leu Thr
224          180         185         190
225      Leu Arg Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys
226          195         200         205
227      Tyr Ser Asp Cys Ala Trp Glu Val Val Arg Met Glu Ile Met Lys Ser
228          210         215         220
229      Leu Phe Leu Ser Thr Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg
230          225         230         235         240
231      Asp Leu Gly Ser Ser
232          245
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234 <211> LENGTH: 189
235 <212> TYPE: PRT
236 <213> ORGANISM: Homo sapiens
237 <400> SEQUENCE: 7
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240      Lys Ser Ile Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Ser Leu
241          20          25          30
242      Gly Asn Arg Arg Ala Leu Ile Leu Leu Gly Gln Met Gly Arg Ile Ser
243          35          40          45
244      Pro Phe Ser Cys Leu Lys Asp Arg His Asp Phe Arg Ile Pro Gln Glu

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